Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-32 (cancelled)

33. (Currently Amended) A method for generating a secondary library of protein variants of a target protein comprising:

a) inputting the coordinates of said target protein into a computer;

b) identifying a list of variable residue positions in said target protein;

c) ~~b) utilizing~~ applying a scoring function to said list of variable residue positions in said target protein to generate a ~~filtered set of~~ primary library comprising optimized ~~primary~~ variant protein sequences filtered for desired properties;

d) ~~c) generating~~ identifying a second list of ~~primary variant~~ variable residue positions and amino acids at said variable residue positions in said ~~primary~~ variant protein sequences in said primary library;

e) ~~d)~~ combining a plurality of said variable residue positions in said ~~primary variant~~ second list of variable residue positions to generate a second set of variant protein sequences, ~~secondary library of secondary sequences~~; and

f) ~~e)~~ synthesizing a plurality of ~~secondary sequences~~ said second set of variant sequences to generate said secondary library of protein variants of said target protein, wherein at least one member of said secondary library is not found in said primary library.

34. (Currently Amended) A method according to claim 33 wherein said combining comprises:

~~a)~~ i) generating a set of oligonucleotide probes each encoding at least one of said variant amino acid residues;

~~b)~~ ii) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding at least one of said second set of variant sequences ~~secondary variant proteins~~; and,

~~c)~~ iii) producing said secondary library ~~variant proteins~~ in host cells transformed with said oligonucleotide sequences.

35. (Previously Presented) A method according to claim 33, wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

36. (Previously Presented) A method according to claim 33 wherein said step b) utilizes Protein Design Automation to computationally generate said optimized primary variant sequences.

37. (Previously Presented) A method according to claim 33 wherein said generating of said primary variant positions is by using a probability distribution table.

38. (Previously Presented) A method according to claim 33 wherein said combining of said primary variant positions is by using a probability distribution table.

39. (Previously Presented) A method according to claim 33 wherein said combining is done computationally.

40. (Previously Presented) A method according to claim 33 wherein said combining and synthesizing are done simultaneously using gene shuffling.

41. (Previously Presented) A method according to claim 33 wherein said combining and synthesizing are done simultaneously using multiple PCR with pooled oligonucleotides.